

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Lal, Preeti
Corley, Neil C.
Tang, Y. Tom

(ii) TITLE OF THE INVENTION: AUTOANTIGEN-LIKE PROTEIN

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0385 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 395 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: HUVENOB01
(B) CLONE: 35842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Phe Pro Arg Val Ser Thr Phe Leu Pro Leu Arg Pro Leu Ser Arg
 1 5 10 15
 His Pro Leu Ser Ser Gly Ser Pro Glu Thr Ser Ala Ala Ala Ile Met
 20 25 30
 Leu Leu Thr Val Arg His Gly Thr Val Arg Tyr Arg Ser Ser Ala Leu
 35 40 45
 Leu Ala Arg Thr Lys Asn Asn Ile Gln Arg Tyr Phe Gly Thr Asn Ser
 50 55 60
 Val Ile Cys Ser Lys Lys Asp Lys Gln Ser Val Arg Thr Glu Glu Thr
 65 70 75 80
 Ser Lys Glu Thr Ser Glu Ser Gln Asp Ser Glu Lys Glu Asn Thr Lys
 85 90 95
 Lys Asp Leu Leu Gly Ile Ile Lys Gly Met Lys Val Glu Leu Ser Thr
 100 105 110
 Val Asn Val Arg Thr Thr Lys Pro Pro Lys Arg Arg Pro Leu Lys Ser
 115 120 125
 Leu Glu Ala Thr Leu Gly Arg Leu Arg Arg Ala Thr Glu Tyr Ala Pro
 130 135 140
 Lys Lys Arg Ile Glu Pro Leu Ser Pro Glu Leu Val Ala Ala Ala Ser
 145 150 155 160
 Ala Val Ala Asp Ser Leu Pro Phe Asp Lys Gln Thr Thr Lys Ser Glu
 165 170 175
 Leu Leu Ser Gln Leu Gln Gln His Glu Glu Glu Ser Arg Ala Gln Arg
 180 185 190
 Asp Ala Lys Arg Pro Lys Ile Ser Phe Ser Asn Ile Ile Ser Asp Met
 195 200 205
 Lys Val Ala Arg Ser Ala Thr Ala Arg Val Arg Ser Arg Pro Glu Leu
 210 215 220
 Arg Ile Gln Phe Asp Glu Gly Tyr Asp Asn Tyr Pro Gly Gln Glu Lys
 225 230 235 240
 Thr Asp Asp Leu Lys Lys Arg Lys Asn Ile Phe Thr Gly Lys Arg Leu
 245 250 255
 Asn Ile Phe Asp Met Met Ala Val Thr Lys Glu Ala Pro Glu Thr Asp
 260 265 270
 Thr Ser Pro Ser Leu Trp Asp Val Glu Phe Ala Lys Gln Leu Ala Thr
 275 280 285
 Val Asn Glu Gln Pro Leu Gln Asn Gly Phe Glu Glu Leu Ile Gln Trp
 290 295 300
 Thr Lys Glu Gly Lys Leu Trp Glu Phe Pro Ile Asn Asn Glu Ala Gly
 305 310 315 320
 Phe Asp Asp Asp Gly Ser Glu Phe His Glu His Ile Phe Leu Glu Lys
 325 330 335
 His Leu Glu Ser Phe Pro Lys Gln Gly Pro Ile Arg His Phe Met Glu
 340 345 350
 Leu Val Thr Cys Gly Leu Ser Lys Asn Pro Tyr Leu Ser Val Lys Gln
 355 360 365
 Lys Val Glu His Ile Glu Trp Phe Arg Asn Tyr Phe Asn Glu Lys Lys
 370 375 380
 Asp Ile Leu Lys Glu Ser Asn Ile Gln Phe Asn
 385 390 395

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: HUVENOB01
 (B) CLONE: 35842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GACGTGTTG	GCAGCGGGAC	GCACCATTTC	AGTTGTGTC	TTGGTTCATT	TCGTGTCTCG	60
GCGATGTTTC	CTAGACTCTC	GACGTTCTA	CCTCTTCGCC	CCCTTCCCG	CCACCCCTTG	120
TCCTCTGGAA	GCCCAGGAGAC	ATCAGCGGCT	GCGATTATGC	TACTCACTGT	TCGGCACGGA	180
ACAGTCAGGT	ACCGCAGTTC	AGCGCTGTTG	GCCCAGACAA	AAAATAACAT	CCAAAGATAT	240
TTTGGCACTA	ACAGTGTGAT	CTGTAGCAAG	AAAGATAAGC	AGTCTGTTCG	AACTGAGGAG	300
ACTTCCAAGG	AGACTTCAGA	GAGCCAAGAC	AGTGAAAAGG	AAAATACGAA	AAAAGACTTG	360
TTAGGCATTA	TTAAGGGCAT	GAAAGTTGAA	TTAAGCACAG	TAAATGTACG	AAACAACAAAG	420
CCCCCCAAAA	GAAGACCACT	AAAAGTTTG	GAAGCTACAC	TTGGCAGGCT	TCGAAGAGCT	480
ACAGAATATG	CTCCAAAGAA	GAGAATTGAG	CCCTTGAGTC	CTGAGTTGGT	GGCAGCTGCA	540
TCTGCTGTGG	CAGATTCTCT	CCCTTTGAT	AAGCAAACAA	CCAAGTCAGA	GCTGCTGAGC	600
CAGCTCCAGC	AGCATGAGGA	AGAGTCAGG	GCACAGAGAG	ATGCAAAGCG	ACCTAAAATT	660
AGTTTCAGTA	ACATAATATC	AGATATGAAA	GTTGCCAGAT	CTGCTACAGC	TAGAGTTCGT	720
TCAAGACCAAG	AGCTTCGGAT	TCAGTTGAT	GAAGGCTATG	ACAATTATCC	TGGCCAGGAG	780
AAGACGGATG	ATCTTAAAAAA	AAGGAAAAAT	ATATTACAG	GGAAAAGACT	TAATATTTT	840
GACATGATGG	CAGTTACTAA	AGAACGACCT	GAAACAGACA	CATCACCCITC	ACTTTGGGAT	900
GTGGAATTG	CTAACGAGTT	AGCCACAGTA	AATGAACAAAC	CCCTTCAGAA	TGGATTTGAA	960
GAGCTGATCC	AGTGGACAAA	AGAGGGAAA	CTATGGGAGT	TCCCAATTAA	CAATGAAGCA	1020
GGTTTGATG	ATGATGGTTC	AGAATTTCAT	GAACATATAT	TTCTGGAGAA	ACACCTGGAG	1080
AGCTTTCCAA	AAACAAGGACC	AATTGCCAC	TTCATGGAGC	TGGTGAATTG	TGGCCTTTCC	1140
AAAAACCCAT	ATCTTAGTGT	TAACACAGAAG	GTTGAACACAA	TAGAGTGGTT	TAGAAATTAT	1200
TTTAATGAAA	AAAAGGATAT	TCTAAAAGAA	AGTAACATAC	AGTTCAATTA	AGACCATGGA	1260
AATTTTATT	TCAAACAATT	AGAGATGGAT	ATTACAACTA	AATAAAATAA	TTGC	1314

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: GenBank
 (B) CLONE: 1272669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Leu	His	Arg	Ile	Pro	Ala	Phe	Leu	Arg	Pro	Arg	Pro	Phe	Ser	Gly
1				5				10				15			
Leu	Pro	Leu	Ser	Cys	Gly	Asn	Arg	Asp	Val	Ser	Val	Ala	Val	Leu	Pro
				20				25				30			
Ala	Ala	Gln	Ser	Gly	Ala	Val	Arg	Thr	Glu	Asn	Asn	Ile	Gln	Arg	His
				35				40				45			
Phe	Cys	Thr	Ser	Arg	Ser	Ile	Cys	Ser	Lys	Lys	Val	Asp	Gln	Ser	Val
				50				55			60				
Pro	Ala	Asn	Glu	Ile	Ser	Gln	Lys	Ala	Ala	Glu	Ser	Gln	Gly	Arg	Gly
				65				70			75			80	
Lys	Glu	Thr	Leu	Lys	Lys	Asp	Leu	Leu	Asp	Ile	Ile	Lys	Asp	Met	Lys
				85				90				95			
Val	Asp	Leu	Ser	Thr	Ala	Asn	Val	Lys	Thr	Pro	Lys	Pro	Arg	Gly	Arg
				100				105				110			
Lys	Pro	Ser	Ala	Ser	Leu	Glu	Ala	Thr	Val	Asp	Arg	Leu	Gln	Lys	Ala
				115				120				125			
Pro	Glu	Asp	Pro	Pro	Lys	Lys	Arg	Asn	Glu	Phe	Leu	Ser	Pro	Glu	Leu

130	135	140	
Val Ala Ala Ala Ser Ala Val Ala Asp Ser	Leu Pro Phe Asp Lys Gln		
145	150	155	
Thr Thr Lys Ser Glu Leu Leu Arg Gln	Leu Gln Gln His Glu Glu	Glu	
165		175	
Leu Arg Ala Gln Lys Asp Arg Glu	Lys Arg Arg Ile Ser Phe	Thr His	
180	185	190	
Ile Ile Ser Asn Met Lys Ile Ala Lys	Ser Pro Ser Gly Arg Ala Ser		
195	200	205	
Thr Arg Pro Gln His Gln Ile Gln	Phe Asp Glu Asp Met Asp Ser	Ser	
210	215	220	
Leu Lys Gln Glu Lys Pro Thr Asp Phe	Arg Lys Arg Lys Tyr Leu Phe		
225	230	235	240
Lys Gly Lys Arg Leu Ser Ile Phe Ala	Asp Lys Ala Phe Ala Asp	Glu	
245	250	255	
Pro Pro Glu Pro Glu Ala Ser Pro	Ser Leu Trp Glu Ile Glu Phe	Ala	
260	265	270	
Lys Gln Leu Ala Ser Val Ala Asp Gln	Pro Phe Glu Asn Gly Phe	Glu	
275	280	285	
Glu Met Ile Gln Trp Thr Lys Glu Gly	Lys Leu Trp Glu Phe Pro	Val	
290	295	300	
Asn Asn Glu Ala Gly Leu Asp Asp Asp	Gly Ser Glu Phe His Glu His		
305	310	315	320
Ile Phe Leu Asp Lys Tyr Leu Glu Asp	Phe Pro Lys Gln Gly Pro	Ile	
325	330	335	
Arg Leu Phe Met Glu Leu Val Thr Cys	Gly Leu Ser Lys Asn Pro	Tyr	
340	345	350	
Leu Ser Val Lys Gln Lys Val Glu His	Ile Glu Trp Phe Arg Asn	Tyr	
355	360	365	
Phe Asn Glu Lys Arg Asp Ile Leu Lys	Glu Asn Asn Ile Ala Phe	Thr	
370	375	380	